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*Published in:*  
Journal of the American Chemical Society

*DOI:*  
[10.1021/ja903224q](https://doi.org/10.1021/ja903224q)

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*Document Version*  
Publisher's PDF, also known as Version of record

*Publication date:*  
2009

[Link to publication in University of Groningen/UMCG research database](#)

*Citation for published version (APA):*

Fuhrmans, M., Knecht, V., & Marrink, S. J. (2009). A Single Bicontinuous Cubic Phase Induced by Fusion Peptides. *Journal of the American Chemical Society*, 131(26), 9166-+. <https://doi.org/10.1021/ja903224q>

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**A single bicontinuous cubic phase induced by fusion peptides  
- SUPPLEMENTAL INFORMATION -**

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This supplemental material contains details of the simulation setup and modeling of the peptide, and one additional figure showing the peptide/lipid organization for a larger system.

## 1. Details of the simulation setup

All simulations were carried out with the Gromacs 3.3 simulation package<sup>1</sup> using the standard run-parameters for the MARTINI model<sup>2</sup> at a timestep of 40 fs. The setup for the simulations is similar for all conditions - 256 molecules of DOPE, 4 fusion peptides and between 2 and 3 coarse grained water molecules per lipid (representing actual hydration levels of 8 to 12 water molecules per lipid) and sodium ions (to counter the charges of the peptides) were randomly placed in a cubic simulation box. After a short relaxation run using isotropic pressure coupling in which all non-bonded interactions in the system were set to be similar to those between water beads, the actual simulations were carried out with anisotropic pressure coupling using the Berendsen coupling scheme<sup>3</sup> with a compressibility of  $5 \times 10^{-5} \text{ bar}^{-1}$  for the diagonal elements and  $1 \times 10^{-7} \text{ bar}^{-1}$  for the off-diagonal elements of the pressure tensor, a coupling time constant of 1.2 ps and a reference pressure of 1.0 bar. The temperature was coupled to values from 270 to 315 K using a Berendsen thermostat<sup>3</sup> with a coupling time constant of 0.5 ps. Lennard-Jones and Coulomb interactions were obtained every step for beads within 1.2 nm according to a neighbor list updated every 10 steps. Both the Lennard-Jones and Coulomb potential were modified with a shift function to have the interactions smoothly vanishing at the cut-off. Electrostatic interactions were screened with a dielectric constant of 15. The simulation corresponding to the given images contained 618 coarse grained water beads corresponding to a hydration level of 9.7 water molecules per lipid and was run at 315 K. Results for other parts of the phase diagram will be published elsewhere. Example input topologies and coordinate files can be found at the Martini web-site (<http://md.chem.rug.nl/~marrink/coarsegrain.html>).

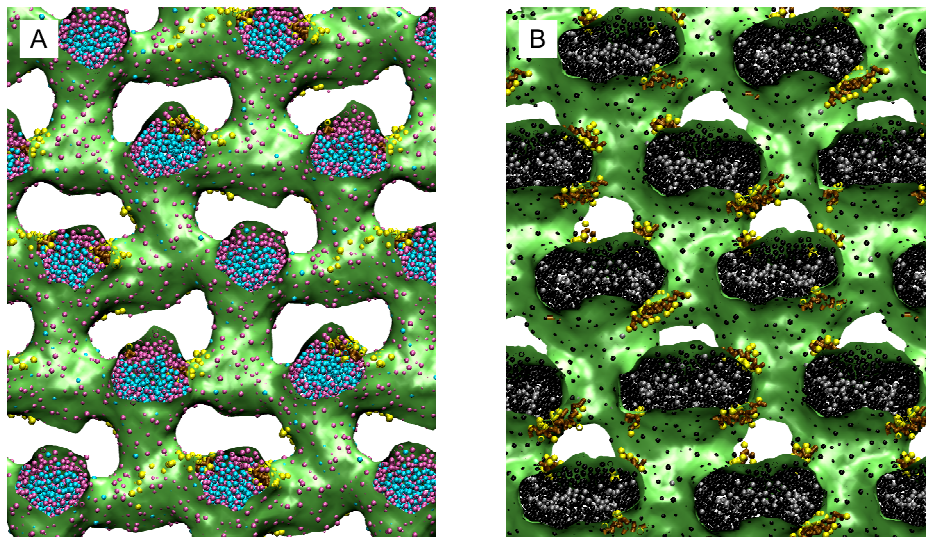
## 2. The model for the fusion peptide

The model for the Influenza HA fusion peptide was optimized to match the 5<sup>th</sup> structure contained in the Protein Data Bank entry 1IBN<sup>4</sup>. Using a preliminary version of the MARTINI model, the parameters were set corresponding to the sequence and a secondary structure alpha-helical from residue 2-10 and 15-18 with a turn for residues 11-14 (DSSP code obtained with the dssp program from the Gromacs package: ~HHHHHHHHHTTTTHHH~). To reproduce the experimental angle between the two helices, additional dihedral angle potentials were introduced for the backbone beads of residue 8 to 16, with a force constant of  $400 \text{ kJ mol}^{-1}$ , a multiplicity of 1 and a minimum at the angles found for the corresponding alpha carbons in the experimental structure. Asp and Glu residues were unprotonated giving the peptide a net charge of -3.

## 3. Snapshot for a bigger system

Using the final configuration of the simulation corresponding to the images given in the manuscript as a template, a bigger system was created by doubling every dimension of

the simulation box and filling the additional volume with duplicates of the original configuration. The resulting system was then simulated for an additional 4  $\mu$ s and remained stable. Fig. 1 shows an additional snapshot of this system at the end of the simulation.



**Figure 1.** A snapshot of a larger system, containing 2048 DOPE lipids and 32 Influenza HA fusion peptides, after 4  $\mu$ s of simulation. Lipid tail beads are shown in grey, glycerol and headgroup beads in magenta, water beads in blue and beads corresponding to the backbone and sidechains of the fusion peptide in brown and yellow, respectively. The surface separating the lipid tail beads from the rest of the system is shown in green, highlighting the three-dimensional networks of the lipid and aqueous components.

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